Version with Markings to Show Changes Made

In the Specification

The paragraph beginning at line 21, page 20, and extending through numbered line 9 on page 21 has been amended as follows:

One advantage of deriving pepscans from genetic material is that the sequence of the genetic material does not need to be known. As long as DNA is available, it can be digested and expressed in a phage display library, which can include up to from about ~~10^{10}~~ 10^6 to about 10^{10} phages. The size limitations of such a library easily accommodate even rather large genomes, including those of viruses, bacteria, yeast and parasites. For example, viruses have genomes of from about 10^3 to about 10^4 bp or more. Bacteria have genomes of about 10^6 bp, yeast about 10^7 bp and parasites from about 10^7 bp to about 10^8 bp or more. The size of the library required to accommodate a complete pepscan of the genome of an organism can be calculated according to the following formulas.

$$number\ of\ peptides = \frac{genome\ size}{3}$$

$$chances\ of\ an\ inserted\ fragment\ yielding\ a\ viable\ phage = \frac{1}{3} * \frac{1}{3} * \frac{1}{2}$$

$$number\ of\ phages = \frac{genome\ size * 18}{3} = 6 * genome\ size$$

~~only 1/18 will be viable for an approximately single-fold coverage of the~~ Of the number of phages initially required for insertion of DNA fragments, only 1/18 will be viable for an approximately single-fold coverage of the complete pepscan. Greater coverage, such as from about five- to about ten-fold coverage, is preferable. In any case, a complete pepscan of even the entire genome of a parasite of about 10^8 bp can clearly be accommodated by a single phage display library, since using the above formulas, only about $6*10^8$ phages would be required.

In the Claims

Claims 112-143 have been deleted, and new claims 144-176 have been added.